

RAW SEQUENCE LISTING

Loaded by SCORE, no errors detected.

Application Serial Number: 10609296

Source: OIPE

Date Processed by SCORE: 9/16/2008

ENTERED

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Maxygen Holdings Ltd.
<120> TITLE OF INVENTION: NEW INTERFERON BETA-LIKE MOLECULES
<130> FILE REFERENCE: 0228us410

<140> CURRENT APPLICATION NUMBER: 10609296
<141> CURRENT FILING DATE: 2003-06-27
<150> PRIOR APPLICATION NUMBER: US/10/084,706
<151> PRIOR FILING DATE: 2002-02-26
<150> PRIOR APPLICATION NUMBER: US 60/272,116
<151> PRIOR FILING DATE: 2001-02-27
<150> PRIOR APPLICATION NUMBER: US 60/343,436
<151> PRIOR FILING DATE: 2001-12-21
<150> PRIOR APPLICATION NUMBER: US 60/302,140
<151> PRIOR FILING DATE: 2001-06-29
<150> PRIOR APPLICATION NUMBER: US 60/316,170
<151> PRIOR FILING DATE: 2001-08-30
<150> PRIOR APPLICATION NUMBER: not yet assigned
<151> PRIOR FILING DATE: 2002-02-19
<150> PRIOR APPLICATION NUMBER: DK PA 2001 00333
<151> PRIOR FILING DATE: 2001-03-01
<150> PRIOR APPLICATION NUMBER: US 09/648,569
<151> PRIOR FILING DATE: 2000-08-25
<160> NUMBER OF SEQ ID NOS: 57
<170> SOFTWARE: FastSEQ for Windows Version 4.0

<210> SEQ ID NO 1
<211> LENGTH: 840
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (76)...(636)
<400> SEQUENCE: 1
60 acattctaac tgcaaccttt cgaaggcttt gctctggcac aacaggttgtt aggcgacact
111 gttcgtgttg tcaac atg acc aac aag tgt ctc ctc caa att gct ctc ctg
159 Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu
1 5 10
ttg tgc ttc tcc act aca gct ctt tcc atg agc tac aac ttg ctt gga
207 Leu Cys Phe Ser Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly
15 20 25
ttc cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa
255 Phe Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln
30 35 40
ttg aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac
303 Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp
45 50 55 60
atc cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc

Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala
 351 65 70 75
 gca ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga
 Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg
 399 80 85 90
 caa gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc
 Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu
 447 95 100 105
 ctg gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa
 Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu
 495 110 115 120
 gaa aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt
 Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser
 543 125 130 135 140
 ctg cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc
 Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala
 591 145 150 155
 aag gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta
 Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu
 636 160 165 170
 agg aac ttt tac ttc att aac aga ctt aca ggt tac ctc cga aac
 Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
 696 175 180 185
 tgaagatctc cttagcctgtg cctctggac tggacaattt cttcaagcat tcttcaacca
 gcagatgtg tttaagtgtac tggacttggctaa tggactgtcat atgaaaggac actagaagat
 756 tttgaaattt ttatattttt atgagtttatt ttatattttt taaattttat tttggaaaat
 816 aaattttttt tggcggaaaaa gtca
 840

<210> SEQ ID NO 2
 <211> LENGTH: 166
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: CHAIN
 <222> LOCATION: (1)...(166)
 <223> OTHER INFORMATION: hIFNB mature sequence
 <400> SEQUENCE: 2
 Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
 1 5 10 15
 Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
 20 25 30
 Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
 35 40 45
 Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
 50 55 60
 Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
 65 70 75 80
 Glu Thr Ile Val Glu Asn Leu Ala Asn Val Tyr His Gln Ile Asn
 85 90 95
 His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr

	100	105	110												
Arg	Gly	Lys	Leu	Met	Ser	Ser	Leu	His	Leu	Lys	Arg	Tyr	Tyr	Gly	Arg
			115				120				125				
Ile	Leu	His	Tyr	Leu	Lys	Ala	Lys	Glu	Tyr	Ser	His	Cys	Ala	Trp	Thr
			130			135				140					
Ile	Val	Arg	Val	Glu	Ile	Leu	Arg	Asn	Phe	Tyr	Phe	Ile	Asn	Arg	Leu
	145			150				155			160				
Thr	Gly	Tyr	Leu	Arg	Asn										
			165												

<210> SEQ ID NO 3
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 3
60 ggctagcggtt taaacttaag cttcgccacc atgaccaaca agtgccctgct ccagatcgcc
70 ctgctcctgt

<210> SEQ ID NO 4
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 4
60 acaacacctgct cggcttcctg cagaggagtt cgaacttcca gtgccagaag ctcctgtggc
70 agctgaacgg

<210> SEQ ID NO 5
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 5
60 gaacttcgac atccccgagg aaatcaagca gctgcagcag ttccagaagg aggacgccgc
70 tctgaccatc

<210> SEQ ID NO 6
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 6
60 ttccgccagg actccagctc caccgggtgg aacgagacca tcgtggagaa cctgctggcc
70 aacgtgtacc

<210> SEQ ID NO 7
<211> LENGTH: 70
<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 7
60 aggagaagct ggagaaggag gacttcaccc gcggcaagct gatgagctcc ctgcacctga
70 agcgctacta

<210> SEQ ID NO 8
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 8
60 ggagtagacgc cactgcgcct ggaccatcgt acgcgtggag atcctgcgca acttctactt
70 catcaaccgc

<210> SEQ ID NO 9
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 9
60 caccacactg gactagtgga tccttatcag ttgcgcaggt agccggtcag gcggttgatg
70 aagtagaagt

<210> SEQ ID NO 10
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 10
60 aggcgcagtg gctgtactcc ttggccttca ggtagtgca gatgcggcca tagtagcgct
70 tcaggtgcag

<210> SEQ ID NO 11
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 11
60 ctccttctcc agcttctcct ccagcacggt ctccaggtgg ttgatctgg ggtacacggt
70 ggccagcagg

<210> SEQ ID NO 12
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 12
60 gagctggagt cctggcggaa gatggcgaag atgttctgca gcatctcgta gatggtcaga
70 gcggcgtcct

<210> SEQ ID NO 13
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 13
60 cctcgggat gtcgaagttc atcctgtcct tcaggcagta ctccaggcgc ccgttcagct
70 gccacaggag

<210> SEQ ID NO 14
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 14
60 caggaagccg agcaggttgt agtcatcga tagggccgtg gtgctgaagc acaggagcag
70 ggcgatctgg

<210> SEQ ID NO 15
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 15
60 ctgctccaga tcgcccgtct cctgtgttc agcaccacgg ccctatcgat gaagcaccag
70 caccagcatc

<210> SEQ ID NO 16
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer
<400> SEQUENCE: 16
60 cactgcttac tggcttatcg aaatataac gactcactat agggagaccc aagctggcta
70 gcgtttaaac

<210> SEQ ID NO 17
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE: